

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/218,913A

DATE: 01/12/2001  
TIME: 10:23:22

Input Set : A:\Pto.amc  
Output Set: N:\CRF3\01112001\I218913A.raw

212 Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met  
213 35 40 45  
215 Leu Arg Cys  
216 50  
218 <210> SEQ ID NO: 8  
219 <211> LENGTH: 92  
220 <212> TYPE: PRT  
221 <213> ORGANISM: Homo sapien  
223 <400> SEQUENCE: 8  
224 Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val  
225 1 5 10 15  
227 Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr  
228 20 25 30  
230 Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser  
231 35 40 45  
233 Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val  
234 50 55 60  
236 Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp  
237 65 70 75 80  
239 Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser  
240 85 90  
242 <210> SEQ ID NO: 9  
243 <211> LENGTH: 708  
244 <212> TYPE: DNA  
245 <213> ORGANISM: Homo sapien  
247 <220> FEATURE:  
248 <221> NAME/KEY: misc\_feature  
249 <222> LOCATION: 679..708  
250 <223> OTHER INFORMATION: /note= "n at positions 622, 679, 707 is any nucleic acid"  
252 <400> SEQUENCE: 9  
253 ggccgggtcg tttctcgccg ggtctggatc gctgtccctc tctggggcc tggcgccgca 60  
255 ccgagaaacgc agcacccacq acttctgcct ggtgtcgaaq gtgggtggca gatgccgggc 120  
257 ctccatgcct aggtgtgtt acaatgtcac tgacggatcc tgccagctgt ttgtgtatgg 180  
259 gggctgtqac ggaaacacgca ataattacct gccaaggag gatgtgcctca aaaaatgtgc 240  
261 caactgtcaca gagaatgcac cgggtgaccc ggcacccagc aggaatgcac cggattcc 300  
263 tgcccaactg gtcctccagaa ggcaggattc tgaagaccac tccagcgata tggtaacta 360  
265 tgaagaataac tgccacccca acgcacgtcac tgggccttgc cgtgcacatct tccccacgctg 420  
267 gtacttttgcgtt gttggagatggaa actctgtcaa taacttcatc tatggaggct gccggggca 480  
269 taagaacacgc taccgcctg aggaggctg catgtccgc tgcttccggcc agcaggagaa 540  
271 tccctccctg ccccttggct caaagggtggat ggttctggcc ggggctgttt cgtgatggtg 600  
273 ttgatccctt tccctggggag cintccatgtt cttaactgatt cccgggtggca aggaggaacc 660  
275 aggagcgtgc cctgcgganc gtctggatgtc tccggatgtca aagggtt 708  
277 <210> SEQ ID NO: 10  
278 <211> LENGTH: 235  
279 <212> TYPE: PRT  
280 <213> ORGANISM: Homo sapien  
282 <220> FEATURE:  
283 <221> NAME/KEY: peptide  
284 <222> LOCATION: 1..235

see next page

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285 <223> OTHER INFORMATION: /note= "Xaa at positions 201, 226, and 233 are nonsense or stop codons"  
 287 <400> SEQUENCE: 10  
 288 Ala Gly Ser Phe Leu Ala Trp Leu Gly Ser Leu Leu Leu Ser Gly Val  
 289 1 5 10 15  
 291 Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser  
 292 20 25 30  
 294 Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn  
 295 35 40 45  
 297 Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly  
 298 50 55 60  
 300 Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala  
 301 65 70 75 80  
 303 Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala  
 304 85 90 95  
 306 Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp  
 307 100 105 110  
 309 His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala  
 310 115 120 125  
 312 Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val  
 313 130 135 140  
 315 Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn  
 316 145 150 155 160  
 318 Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg  
 319 165 170 175  
 321 Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu  
 322 180 190  
 W--> 324 Ala Gly Ala Val Ser Xaa Trp Cys Xaa Ser Phe Ser Trp Gly Ala Ser  
 325 195 200 205  
 327 Met Val Leu Leu Ile Pro Gly Gly Lys Glu Glu Pro Gly Ala Cys Pro  
 328 210 215 220  
 W--> 330 Ala Xaa Arg Leu Glu Leu Arg Arg Xaa Gln Gly  
 331 225 230 235  
 333 <210> SEQ ID NO: 11  
 334 <211> LENGTH: 179  
 335 <212> TYPE: PRT  
 336 <213> ORGANISM: HOMO sapien  
 338 <220> FEATURE:  
 339 <221> NAME/KEY: peptide  
 340 <222> LOCATION: 1..170  
 341 <223> OTHER INFORMATION: /note= "Xaa at positions 8, 17, 19, 21-26, 40, 42, 45-47, 52, 64, 103, 112, 114, 116-121, 135, 137, 140-142, 147, and 159 is any amino acid residue"  
 342 103, 112, 114, 116-121, 135, 137, 140-142, 147, and 159 is any amino acid residue"  
 343  
 345 <400> SEQUENCE: 11  
 W--> 346 Ala Asp Arg Glu Arg Ser Ile Xaa Asp Phe Cys Leu Val Ser Lys Val  
 347 1 5 10 15  
 349 Xaa Gly Xaa Cys Xaa Xaa Xaa Xaa Xaa Trp Trp Tyr Asn Val Thr  
 350 20 25 30  
 W--> 352 Asp Gly Ser Cys Gln Leu Phe Xaa Tyr Xaa Gly Cys Xaa Xaa Xaa Ser  
 353 35 40 45

invalid use of Xaa

Xaa can only represent a single amino acid, nothing else. \*

what about Xaa at position 198?

\*FYI, per 1.822(5)(e) of new Sequence Rules, "a sequence with a gap or gaps shall be presented as a plurality of separate sequences..."

OK

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.